

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 19:52:11 : Search time 49.48 Seconds
(without alignments)
219.297 Million cell updates/sec

Title: US-09-481-990-2

Perfect score: 1753

Sequence: 1 MQLSLAGSSCVRLVERHRSR.....QNE?FVATQSSACVDPANH 336

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222.5	12.7	335	1 TWK8_CAEEL	P34410 caenorhabd
2	178	10.2	691	1 TOK1_YEAST	P0310 saccharomyc
3	138	7.9	228	1 YMS1_CAEEL	Q10937 caenorhabd
4	121	6.9	333	1 Y13B_MERJA	Q57604 methanococc
5	116	6.6	417	1 KCH_ECOLI	P31069 escherichia
6	105	6.0	209	1 Y139_MERJA	Q37603 methanococc
7	100.5	5.7	393	1 NUPC_BACSU	P39141 bacillus su
8	97.5	5.6	356	1 YUXJ_BACSU	P07600 bacillus su
9	97	5.5	802	1 C1KB_RAT	P50052 rattus norv
10	95.5	5.4	363	1 AG22_HUMAN	P15387 homo sapien
11	95	5.4	853	1 C1KA_RAT	P15387 homo sapien
12	95	5.4	854	1 C1KA_HUMAN	Q14721 homo sapien
13	94.5	5.4	363	1 AG22_MOUSE	P35374 mus musculu
14	94.5	5.4	363	1 AG22_RAT	P35374 rattus norv
15	94	5.4	695	1 C1Q4_HUMAN	P56696 homo sapien
16	94	5.4	806	1 C1KB_HUMAN	Q92953 homo sapien
17	93.5	5.3	1174	1 C1EB_BACTA	Q03745 bacillus th
18	93	5.3	718	1 STJ3_YEAST	P39007 saccharomyc
19	92.5	5.3	363	1 AG22_MERUN	Q9206 meriones un
20	92	5.2	343	1 YD57_MERJA	Q8752 methanococc
21	91.5	5.2	663	1 CYOB_ECOLI	P18401 escherichia
22	91.5	5.2	674	1 TM1L_ARATH	P33543 arabidopsis
23	91.5	5.2	1159	1 HERG_HUMAN	Q12809 homo sapien
24	91.5	5.2	1174	1 C1KE_DROME	Q02280 drosophila
25	90.5	5.2	546	1 MUP3_YEAST	P38754 saccharomyc
26	90.5	5.2	580	1 P69_MYCAR	P15362 mycoplasma
27	90.5	5.2	2009	1 C1NL_RAT	P04774 rattus norv
28	90	5.1	899	1 YA8D_SCHPO	Q09778 schistosach
29	89.5	5.1	421	1 CDS1_ARATH	Q04928 a phosphati
30	89.5	5.1	872	1 C1Q3_HUMAN	Q43525 homo sapien
31	89.5	5.1	2223	1 CCAE_DISOM	P56699 discoppyge o
32	89	5.1	350	1 FLHB_AQUAE	Q67813 aquifex aeo
33	89	5.1	388	1 YUBA_BACSU	Q32086 bacillus su

34	89	5.1	425	1 LIVM_ECOLI	P22729 escherichia
35	89	5.1	614	1 YDNK_LACTIC	P42377 lactococcus
36	88.5	5.0	484	1 ALRP_ECOLI	P75712 escherichia
37	88	5.0	425	1 LIVM_SALTY	P30236 salmonella
38	88	5.0	466	1 GABP_ECOLI	P25527 escherichia
39	87.5	5.0	415	1 GSCB_ECOLI	P30000 escherichia
40	87.5	5.0	470	1 CYCA_ECOLI	P39312 escherichia
41	87.5	5.0	518	1 GITL_YEAST	P25346 saccharomyc
42	87.5	5.0	624	1 PPS1_HUMAN	Q43252 h bifunctio
43	87.5	5.0	924	1 C1KB_DROME	P17970 drosophila
44	87	5.0	672	1 CYOB_PSEPU	Q9WR2 pseudomonas
45	86.5	4.9	459	1 Y226_MYCGE	P47468 mycoplasma

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	AA
1	TWK8_CAEEL	1 TWK8_CAEEL	STANDARD	PRT	335 AA
AC	P34410	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	15-JUL-1998	(Rel. 36, Last annotation update)			
DE	TWK-8 PROTEIN				
GN	TWK-8 OR F22B7.7				
OS	Caenorhabditis elegans				
OC	Eukaryota; Metazoa; Nematoa; Chromadorea; Rhabdilitida; Rhabditoidea;				
OC	Rhabdilitida; Pelodierinae; Caenorhabditis				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-BRISTOL NZ;				
RX	MEDLINE-94150718; PubMed-7906398;				
RA	Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,				
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,				
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,				
RA	Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,				
RA	Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,				
RA	Larrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,				
RA	Parsons J., Percy C., Rifkin L., Roopra A., Saunders E., Showkeen R.,				
RA	Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,				
RA	Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,				
RA	Waterson R., Watson A., Weinstock L., Wilkinson-Sproot J.,				
RA	Woldman P.				
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.				
RT	elegans."				
RL	Nature 368:32-38(1994).				
CC	-1- SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.				
CC	-----				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; L12018; AAA65460.1; -				
DR	WORMPDP; F22B7.7; CE00160.				
SO	SEQUENCE 335 AA; 38472 MW; 27DEF1E79B3CA29 CRC64;				
Query Match 12.7%; Score 222.5; DB 1; Length 335;					
Best Local Similarity 27.0%; Pred. No. 5.3e-10;					
Matches 62; Conservative 50; Mismatches 63; Indels 55; Gaps 9;					
QY	92	VLNSAGNMWMDPFASTVSTGTGVTPLPSDGRKACFIYISYIGPFLTFLTA 151			
DB	19	VKNKATE-TWTFSSSIFFAVTVTTIGVGNPVTNIGRWLCIFSLGIPLVLTAD 77			
QY	152	VVORTVHTVTRRPVLYFHIRM-----GF-----SKQVVA-IV 182			
DB	78	LGFLESHLVWLVYGNVYLKTLKTLISRHKKREHVCHEHSHGMDHNIEKRIPALV 137			

QY 183 HAVILGCVTVSCFFPIPAVSVLEDDWNLSEFFCFISLSTIGLDYVPGEGYNOKR 242
 Db 138 LALLIVYTARG-----GVLMKSLF-PWSEFVSFWSTMTTGVGDLMFR-----R 183
 QY 243 ELKICITVGLIGLILAML-----VLETFC-ELHEUKKRRMPY 281
 Db 184 DGMVITLITLIGKFSMKKOKKFKLIGLITTCIDLVGVQYIKIRHY 233
 RESULT 2
 TOK1 YEAST
 ID TOK1 YEAST STANDARD: PRT: 691 AA.
 AC P40310: 005721:
 DE 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTWARD-RECTIFIER POTASSIUM CHANNEL TOK1 (TWO-DOMAIN OUTWARD RECTIFIER
 K+ CHANNEL YORK).
 GN TOK1 OR DUK1 OR YIL093C OR J0911.
 OS Saccharomyces cerevisiae (Baker's yeast).
 Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 Saccharomycetaceae; Saccharomyces.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE-95076716; PubMed-7985424;
 RA Miosga T., Witzel A., Zimmermann F.K.;
 RT "Sequence and function analysis of a 9.46 kb fragment of
 RL Saccharomyces cerevisiae chromosome X.";
 RN Yeast 10:965-973(1994).
 [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-NY13;
 RX MEDLINE-95379951; PubMed-7651518;
 RA Ketchum K.A., Joiner W.J., Sellers A.J., Kaczmarek L.K.,
 RT Goldstein S.A.N.;
 RT "A new family of outwardly rectifying potassium channel proteins with
 RL two pore domains in tandem.";
 RN Nature 376:690-695(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96303826; PubMed-8723646;
 RA Reid J.D., Lukes W., Shafatlian R., Bertl A., Scheurmann-Kettner C.,
 RT Guy H.R., North R.A.;
 RT "The S. cerevisiae outwardly-rectifying potassium channel (DUK1)
 RL identifies a new family of channels with duplicated pore domains.";
 RN Recept. Channels 4:51-62(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RC Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M.,
 RL Romey G., Barhanin J.;
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: OUTWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: SEEM TO BE COMPOSED OF TWO PORES.
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 CC -----
 CC EMBL: X77087; CA54360.1;
 CC EMBL: Z49368; CA869386.1;
 CC EMBL: U28005; AAC49070.1;
 CC EMBL: X94403; CA64176.1;
 CC EMBL: U37254; AAC49168.1;
 CC PIR: S46585; S46585.
 CC PIR: S47058; S47058.
 CC SGD: S0003629; TOK1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel.
 FT TRANSMEM 72 92 S1 (POTENTIAL).
 FT TRANSMEM 138 158 S2 (POTENTIAL).
 FT TRANSMEM 171 191 S3 (POTENTIAL).
 FT TRANSMEM 204 224 S4 (POTENTIAL).
 FT TRANSMEM 247 266 S5 (POTENTIAL).
 FT TRANSMEM 302 322 S6 (POTENTIAL).
 FT TRANSMEM 380 400 S7 (POTENTIAL).
 FT TRANSMEM 436 456 S8 (POTENTIAL).
 FT CONFLICT 442 442 A -> T (IN REF. 3).
 FT CONFLICT 512 512 E -> G (IN REF. 3).
 SO SEQUENCE 691 AA; 77407 MW; 507167E487B77AAE CRC64;

Query Match 10.2%; Score 178; DB 1; Length 691;
 Best Local Similarity 25.4%; Pred. No. 2,7e-06;
 Matches 51; Conservative 33; Mismatches 71; Indels 46; Gaps 6;
 QY 97 SGAMNDFTSALFPASTVSTGYGHTVPLSDGKACFIYVIGIPFLFPAVORI 156
 Db 267 SGLHITYGALFYCVSLTWGLDILKPSVGAKIMVLIFSLGSV--VLMGLYFMTR 324
 QY 157 TVHTRRPVLYFH-IRMGFSKO-----VVAI 181
 Db 325 IICKSSGPIFFPHRVKSGSKSKHMOSSKNLSEREAFLDKCITROTASRKOHWSLSV 384
 QY 182 HAVILGCVTVSCFFPIPAVSVLEDDWNLSEFFCFISLSTIGLDYVPGEGYNOKF 241
 Db 385 TIAIFM-----AFWILGALVFKEAE-NWSYFNCFYFCILITIGYDYDAPRIGAGRAF 437
 QY 242 RELYKIGICVYLLGLILAMLV 262
 Db 438 FYIWMALG-AVPLMKALLSTV 456

RESULT 3
 YWS1 CAEEL
 ID YWS1 CAEEL STANDARD: PRT: 228 AA.
 AC O10937:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE HYPOTHELTICAL 25.6 KDA PROTEIN B0310.1 IN CHROMOSOME X.
 GN B0310.1.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RL Favellio T.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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 CC -----
 CC EMBL: U40959; AAA81765.1;
 CC MORPEP: B0310.1; CE03874.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 107 127 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 188 208 POTENTIAL.
 SO SEQUENCE 228 AA; 25625 MW; 0822E836B3CA2360 CRC64;

Query Match 7.9%; Score 138; DB 1; Length 228;
 Best Local Similarity 23.7%; Pred. No. 0.00085;

Matches 50; Conservative 45; Mismatches 68; Indels 48; Gaps 10;

QY 70 LSEQLLEPFLGRVLEASNYGVSLNAGNNMDFTSLFPAFVTLSTGCHYPLSDG 129
 DB 52 LADOLELTERALLO--HYGDLDKRS-----DKSPASGLORSFAISTTIGPLVDDEFTTL 104
 QY 130 GKAECIIYGVIGIPFTLLEFLAVVQRTIVVHTRRPVLVFLHFKSGSKOVAVIHAVLLGF 189
 DB 105 GKLANVIALGTP---LFLVIVGO-----LGKAVTSWGCTTLM 142
 QY 190 VTSCEFFIPPAVSVLE---DWMNFLESFYCFISLSTIGLADYVPEGYNQKRELYK 246
 DB 143 VTI-VYIFISAVIYDIVGSDVDYFEIAIFSIPLQFTTGEVD-----NEFHG 190
 QY 247 IGITCYLLGLIAMLVLETFCCL-HELKKE 276
 DB 191 VLPYCIIVLGL-ALITAL--YQEMOHNIERF 218

RESULT 4
 ID Y13B_METUA STANDARD; PRT: 333 AA.
 AC 057604;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE POTASSIUM CHANNEL PROTEIN M00138.1.
 GN M00138.1.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 NC Methanococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerecavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Metzler J.M., Nguyen D.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fultman J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sacow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.F., Venter J.C.;
 "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: STRONG, TO M.JANNASCHII M01357.
 CC -1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
 CC -----
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 CC -----
 DR EMBL: U67471; AAB98130.1; -;
 DR TIGR: M0138.1; -;
 KM Hypothetical protein; Transmembrane; Transport; Ion transport;
 FT Ionic channel. 7
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 333 AA; 37149 MM; 7CC082675F96B06A CRC64;
 SO SEQUENCE

Query Match 6.9%; Score 121; DB 1; Length 333;
 Best Local Similarity 26.4%; Pred. No. 0.025;
 Matches 38; Conservative 25; Mismatches 63; Indels 18; Gaps 6;
 QY 187 LGFVTVSCFFIIPPAVSVLEDDNNLFSEFYCFISLSTIGLADYVPEGYNQKRELYK 246

DB 9 LGIIVIIILLILESVIIMTVE-GMDFTAFTAVTISTVIGDGTTP-----QTF--LGK 60
 QY 247 IGITCYLLGLIAMLVLETFCCLHELKFRKMFYKKDKDE---DQVHIEHDLSFS 302
 DB 61 LSVIITIFAGVAVAYVTGNIAISFEIGHFRKRYFLRKMRIKLNHYYIT----CGYG 116
 QY 303 SITDPAAGMKEDQKNEPFAVATQS 326
 DB 117 RLGRVIA--EERFKCNIPFVIIDS 138

RESULT 5
 ID KCH_ECOLI STANDARD; PRT: 417 AA.
 AC P31069; P94716; P94717; P94723; P94729; P97198; P97225;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE POTASSIUM CHANNEL PROTEIN.
 GN KCH.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 NC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=94224769; PubMed=8170937;
 RA Milkman R.;
 RT "An Escherichia coli homologue of eukaryotic potassium channel
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3510-3514(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12, AND VARIOUS ECOR STRAINS;
 RA Milkman R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / M31655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.R.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE DEFENSE AGAINST OSMOTIC SHOCK.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (POTENTIAL).
 CC -1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
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Query Match	Similarity	6.6%	Score 116	DB 1	Length 417
Best Local	Similarity 22.5%		Pred. No. 0.075		
Matches 77	Conservative 46		Mismatches 123	Indels 96	Gaps 15

Query	11	VLVRHRSAMCGFLVGLYLIVE	-----	GAVFSVLEPYEDLLRQELRK	58
Db	79	IGLFRALWAIISILL	-LIALITYLHFYPMLFKSIFCIFTLLVFL	-ILRRDF	131
Db	59	LKRRLHEHCISEQDLQFUG	-RVLEASNGSVLSAASNMWMDTSALEFASVYS		116
Db	132	-----SHSAAAGTITAFISFTLLTYSTYGALYLSGGEFPRIESLMTAFYSLETMS			184
Db	117	TTGYGHTVPLSDGGRACFIIVSVIGIPTLLFLAVVORITVHTRRPYLYPH	-IRWGS		175
Db	185	TVGYGDIVPVESEARLEFI	-----SVIISGIVFAFMSMTSIFPLIRNGEN		230
Qy	176	KOVAVIHAVVLIGFTVSCFEFIPA	-----AVFSLEDDMNLFESYFEC		220
Db	231	KLVGNNTHTMRKDHFIYCGHSILAINITLQNGQNTVYISNLPEDDKOLEO	-----		285
Qy	221	ISLSTIGL	--DYVPGSGYNOKFRELYKIGI	-TCYLLIGLI	263
Db	286	-----RLGDNDADVIPGDSNDSV	-LKKAGIDRCRAITLSDNDADNAFVLSAKDMS		337
Qy	264	-LEFCECELHELKFRKMEYVKKDKREDQVHILEHOLSSST			304
Db	338	DVKITVLAVSDSKNLKIRKHPD	-----ITLSPOLGESET		372

RESULT	6	Y139_METUA	Y139_METUA	STANDARD	PRT	209 AA
AC	057603					
DT	01-NOV-1997	(Rel. 35, Created)				
DT	01-NOV-1997	(Rel. 35, Last sequence update)				

DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0139.
GN MJ0139.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-6880887;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kereyague A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Meldrum J.F., Fuhrman J.L., Nguyen D.,
RA Urrutack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klank H.-P., Friser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: SOME, TO POTASSIUM CHANNEL PROTEINS.
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[illegible]

CC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=96134975; PubMed=8550462;
 RA Saxild H.H., Andersen L.N., Hammer K.;
 RT "Dra-nupc-pdp operon of Bacillus subtilis: nucleotide sequence,
 induction by deoxyribonucleosides, and transcriptional regulation by
 the deor-encoded deor repressor protein.";
 RL J. Bacteriol. 178:424-434(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / BGSC11;
 RX MEDLINE=97021444; PubMed=8667804;
 RA Yoshida K.-I., Fujimura M., Yanai N., Fujita Y.;
 RT Cloning and sequencing of a 23-kb region of the Bacillus subtilis
 genome between the *iol* and *hut* operons.";
 RL DNA Res. 2:295-301(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE SIC28A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL: X82174; CA57663.1; -;
 DR EMBL: D45912; BAA08338.1; -;
 DR EMBL: 299124; CAB15977.1; -;
 DR SUBTILIST: BG10984; NUPC.
 DR INTERPRO: IPR002688; -;
 DR PFAM: PF01773; Nucleoside_ttra2; 1.
 KW Transport; Transmembrane.
 FT TRANSMEM 3 23 POTENTIAL.
 FT TRANSMEM 32 52 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 168 188 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 249 269 POTENTIAL.
 FT TRANSMEM 272 292 POTENTIAL.
 FT TRANSMEM 335 355 POTENTIAL.
 FT TRANSMEM 372 392 POTENTIAL.
 FT TRANSMEM 16 16 F -> L (IN REF. 2).
 FT CONFLICT 304 305 SI -> RL (IN REF. 1).
 FT CONFLICT 320 320 S -> V (IN REF. 1).
 SQ SEQUENCE 393 AA; 42529 MW; C28677B5D30AE0AC CRC64;

Query Match 5.7%; Score 100.5; DB 1; Length 393;
 Best Local Similarity 25.0%; Pred. No. 1;
 Matches 56; Conservative 32; Mismatches 89; Indels 47; Gaps 10;

OY 27 VLGVLVYVFGAVVSSVELPY-----EDLRQELRKRRRLERHELSQQLQEQF LG 80
 DB 193 VVVALVNLVLFEGGFIITASTINIEYAKEDMLRVE-EEEKQSF--EVLGEYILIDGFKVA 248
 OY 81 RVLASNGV--SVLSNAGNMMDFTSALFASVLTSTGYGHTVPLSDGKAFCIITSV 139
 DB 249 VVVAAMLIGFAITALLINGIN-----AVGISFGQILG-----VFAPFAL 291
 OY 140 IGIFPT-----LFLFAVORITVHTRPVLFHTRMGFSKQOVAIVHAVLLGFTVS 193
 DB 292 VGIPWNEAVNAGSIMATKMSNEFVAMSTLRNGFPH---FSGRTTALVSFLVFSFANS 347
 OY 194 CFFFIIPAIVSVLEDDNNFLSEF-----YFCFISLSTIGL 228

DB 348 SIGITAGAVKGLNKGQNVVAFGLKILXGATLVFSLSAAIVGL 391
 RESULT 8
 YUXJ_BACSU STANDARD; PRT; 356 AA.
 ID YUXJ_BACSU
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HYPOTHETICAL 39.1 KDA PROTEIN IN KAPD-PBPD INTERGENIC REGION (ORF1).
 GN YUXJ.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=97419515; PubMed=9274030;
 RA Oudega B., Koningssteijn G., Rodrigues L., de Sales Ramon M.,
 RA Hilbert H., Duesterhoeft A., Pohl T.M., Weitzenecker T.;
 RT Analysis of the Bacillus subtilis genome: cloning and nucleotide
 RT sequence of a 62 kb region between 275 degrees (trnB) and 284 degrees
 RT (pai).";
 RL Microbiology 143:2769-2774(1997).
 RN [2]
 RP SEQUENCE OF 101-356 FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=95050302; PubMed=7961491;
 RA Popham D.L., Setlow P.;
 RT Cloning, nucleotide sequence, mutagenesis, and mapping of the
 RT Bacillus subtilis pbpd gene, which codes for penicillin-binding
 RT protein 4.";
 RL J. Bacteriol. 176:7197-7205(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: STRONG, TO E. COLI YCEE. SOME, TO THE DRUG RESISTANCE
 CC TRANSDUCASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: 293933; CAB07914.1; -;
 DR EMBL: 299120; CAB15137.1; -;
 DR EMBL: U11882; AAA64942.1; -;
 DR SUBTILIST: BG10976; YUXJ.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 119 139 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 201 221 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 SQ SEQUENCE 356 AA; 39105 MW; 31758C0122231311 CRC64;

Query Match 5.6%; Score 97.5; DB 1; Length 356;
 Best Local Similarity 22.0%; Pred. No. 1.6;
 Matches 72; Conservative 34; Mismatches 119; Indels 103; Gaps 12;

OY 3 QSLAGSCVRLVERKRMCFGLVGLV-----LYVFGAVVSSVELPYEDLLRQ 54
 DB 83 KSSAGKTLGTLQMGVSSLSLPGLLGMLADRFGFTYFFTFISFVSLVLFEGVEX 142
 OY 55 EL--RKLRRFLERHEGCS-----EQQLQGLVFLASVNGVSLNAGNMMDFTS 106
 DB 143 HLAETAKRTSRSREVLSYIFHHALVWMLTLTIOTGNFSIOPLLALVYNEHGVN 202


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RC TISSUE-BLOOD:
RX MEDLINE=95032069; PubMed=7945336;
RA Koike G., Horiuchi M., Yamada T., Seprier C., Jacob H.J., Dzau V.J.;
RT "Human type 2 angiotensin II receptor gene: cloned, mapped to the X
RL chromosome, and its mRNA is expressed in the human lung.";
RN Biochem. Biophys. Res. Commun. 203:1842-1850(1994).
RP [4]
RC SEQUENCE FROM N.A.
RX TISSUE-PLACENTA:
RA MEDLINE=94242007; PubMed=8185599;
RT Tsuzuki S., Ichiki T., Nakakubo H., Kitami Y., Izu D.F.,
RA Shurai H., Inagami T.;
RT "Molecular cloning and expression of the gene encoding human
RL angiotensin II type 2 receptor.";
RN Biochem. Biophys. Res. Commun. 200:1449-1454(1994).
RP [5]
RC SEQUENCE FROM N.A.
RX TISSUE-LUNG:
RA MEDLINE=95091796; PubMed=7999093;
RT Martin M.M., Su B., Elton T.S.;
RA "Molecular cloning of the human angiotensin II type 2 receptor cDNA.";
RN Biochem. Biophys. Res. Commun. 205:645-651(1994).
RP [6]
RC SEQUENCE FROM N.A.
RX TISSUE-PLACENTA:
RA MEDLINE=95236034; PubMed=7719706;
RT Lazard D., Briand-Sutren M.M., Villageois P., Mattel M.-G.,
RA Strosberg A.D., Naimias C.;
RT "Molecular characterization and chromosome localization of a human
RL angiotensin II AT2 receptor gene highly expressed in fetal tissues.";
RN Recept. Channels 2:271-280(1994).
RP [7]
RC SEQUENCE OF 1-22 FROM N.A.
RX TISSUE-BLOOD:
RA Katsuya T., Dzau V.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 1-16 FROM N.A.
RX TISSUE-UTERUS:
RA Warnecke C.H., Holmeister J., Regitz-Zagrosek V., Fleck E.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [9]
RP FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
RX MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.
CC [10]
RP SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC [11]
RP TISSUE SPECIFICITY: IN ADULT, HIGHLY EXPRESSED IN MYOMETRIUM WITH
RX LOWER LEVELS IN ADRENAL GLAND AND FALLOPIAN TUBE. VERY HIGHLY
CC EXPRESSED IN FETAL KIDNEY AND INTESTINE.
CC [12]
RP SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: U20860; AAA85851.1; -
DR EMBL: L34579; AAA98990.1; -
DR EMBL: U10273; AAA61794.1; -
DR EMBL: U15592; AAA50762.1; -
DR EMBL: U16957; AAA67753.1; -
DR EMBL: U27478; AAA84900.1; -
DR EMBL: X87723; CAA61022.1; -
DR HSP: P34996; IDDD.
DR GCRDB: GCR_1057; -
DR GCRDB: GCR_1245; -
DR GCRDB: GCR_1876; -
DR GCRDB: GCR_2011; -
DR GCRDB: GCR_2027; -
DR GCRDB: GCR_2031; -
DR GCRDB: GCR_2056; -
DR MIM: 300034; -

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DR	INTERPRO: IP000147; -	-
DR	INTERPRO: IP000248; -	-
DR	INTERPRO: IP000276; -	-
DR	PFAM: PF00001; 7tm_1; 1.	
DR	PRINTS: PR00237; GPCRHHOOPSN.	
DR	PRINTS: PR00241; ANGIOTENSINR.	
DR	PRINTS: PR00636; ANGIOTENSIN2.	
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1.	
DR	PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.	
KW	G-protein coupled receptor; transmembrane; glycoprotein.	
FT	DOMAIN	1 45
FT	TRANSMEM	46 71
FT	DOMAIN	72 80
FT	TRANSMEM	81 102
FT	DOMAIN	103 119
FT	TRANSMEM	120 140
FT	DOMAIN	141 160
FT	TRANSMEM	161 179
FT	DOMAIN	180 208
FT	TRANSMEM	209 234
FT	DOMAIN	235 256
FT	TRANSMEM	257 278
FT	DOMAIN	279 285
FT	TRANSMEM	286 313
FT	DOMAIN	314 363
FT	CARBOHYD	4 4
FT	CARBOHYD	13 13
FT	CARBOHYD	24 24
FT	CARBOHYD	29 29
FT	CARBOHYD	34 34
FT	CONFLICT	268 269
FT	CONFLICT	272 272
FT	CONFLICT	323 323
Q	SEQUENCE	363 AA; 41183 MW; FDDYD4SEGF9543E60 CRC64; N -> G (IN REF. 4); F -> L (IN REF. 4);

Query March	5.48;	Score 95.5;	DB 1;	Length 363;
Best Local Similarity	20.98;	Pred. No. 2.3;		
Matches 60;	Conservative 40;	Mismatches 80;	Indels 107;	Gaps

QY	17	HRSAWCEGFL---	VLGYLLYL-VEGAVF--	SSVELPYEDLLRQELRKLRRELEEH--	67
		: : :	: : :	: : :	
Db	106	YRYDMLPEPVNCKYFGSFLTLNMFASIFITCM	SYVD- RYGSVIYPFLLSQRRNPQASVIY	164	
		: : :	: : :	: : :	
QY	68	-----ECLSEQQLLEQELGRVLEASNY-----		-----GVSYLNASGNNN	101
		: : :	: : :	: : :	
Db	165	PLVYCMACLS--SLPTFEYRDVPTIEYLGNACIMAFPEPKYAAOMSGIALMKNLIS---		219	
		: : :	: : :	: : :	
QY	102	WDFISALFFAST-----	VLSTTGCGHYPLSDG--	GKACIIYSVIGIF- TLIF	148
		: : :	: : :	: : :	
Db	220	--FIIPLEFIATCYEGIRKHLKLTNSYGKNRITBDQYLKMAAAVLAFLITCWLPEHVLTF			277
		: : :	: : :	: : :	
QY	149	LTAAVORTTAVTRRPVLXFIHRGFSKQOVAIY----	HAVLIGFVWSCEFFIPAAVF	203	
		: : :	: : :	: : :	
Db	278	LDALAMGVIN-----	SGEVAIVIDLALPEAFILIGF-TNSC-----	312	
		: : :	: : :	: : :	
QY	204	SVLEDNMNLFSEFYCFISLTSLIGDVPPEGYNOKFRELYKIGIT	250		
		: : :	: : :	: : :	
Db	313	-----VNPFLXCFV-----	GNRRQQRKLSRYFRVPIIT	338	
		: : :	: : :	: : :	

RESULT	11
C1KA_RAT	
C1KA_RAT	STANDARD;
AC	PL5387;
PT	01-APR-1990 (Rel. 14, Created)
DT	01-AUG-1990 (Rel. 15, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DBK1).
GN	KCNB1.
OS	Rattus norvegicus (Rat).
OC	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Scuriongnath; Muridae; Murinae; Rattus


```

[1] SEQUENCE FROM N.A.
RC TISSUE=BRAIN:
RX MEDLINE=69365157; PubMed=2770868;
RA Frech G.C., Vandongen A.M.J., Schuster G., Brown A.M., Joho R.H.;
RT "A novel potassium channel with delayed rectifier properties isolated
RN from rat brain by expression cloning." ;
RP Nature 340:642-645(1989).
RA REVISIONS.
RA Frech G.C.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.
CC -I FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC THE CEREBRAL CORTEX, FOLLOWED BY THE HIPPOCAMPUS, CEREbellum, AND
CC OLFACTORY BULB. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
CC RETINA AND KIDNEY. ALSO PRESENT IN CARDIAC MUSCLE TISSUE OF THE
CC ARTERIAL AND VENTRICLE AND IN SKELETAL MUSCLE.
CC -I DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -I SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
CC EMBL; X16476; CAA34497.1; -.
DR PIR; S05448; CHRDL.
DR INTERPRO; IPRO000636; -.
DR INTERPRO; IPRO003091; -.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00169; KCANNEL.
RV Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
RV Glycoprotein; Multigene family; Phosphorylation.
FT DOMAIN 1 182
FT TRANSMEM 183 204 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 205 224 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 225 246 SEGMENT S2 (POTENTIAL).
FT DOMAIN 247 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 278 SEGMENT S3 (POTENTIAL).
FT DOMAIN 279 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 312 SEGMENT S4 (POTENTIAL).
FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 327 348 SEGMENT S5 (POTENTIAL).
FT DOMAIN 349 388 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 389 410 SEGMENT S6 (POTENTIAL).
FT DOMAIN 411 853 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED GLYCAC. ) (POTENTIAL).
FT MOD_RES 440 440 PHOSPHORYLATION (BY CAPK (POTENTIAL)).
FT MOD_RES 492 492 PHOSPHORYLATION (BY CAPK (POTENTIAL)).
FT SEQUENCE 853 AA; 95280 MW; 7A08998839716165 CRC64;

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OY      13 IVERHSAACFGVLYGLYLLVFGAVSSVSLPEYEDLLRGLRKRREHEHCISE 72
Db      174 LLEKPMSSAAKIALIITISIMFYLSITIALSLNTLP-----ELGSLD----EFGOSTN 222
OY      73 QOLEQFLGAVLEA-----SNYGVSLSNASGNNMWDTSALFFASTVLTGTGYHP 125
Db      223 POLAH-----VEAVCIAMFTMEYLIRFLSSPK---KMKFFKGPLMADILLALIPYVITF 274
OY      126 LSDGGA---FCIIYVIGIPIPTLFLFATVAVORITVHYTRRPLVYHIMWGSKOVAALV 182
Db      275 LTESNSVYLQFQVNRVAVOI-PRIMKILRI-LKLARHSGLOSLGFTLRSYNEL----- 327
OY      183 HAVILGFYVSCFFPIPAVFSVL-EDDNFLE---SPFYCSLTSLTIGVYVPEGYN 238
Db      328 -GLIILFLAMGLMIFSSLVFEAKDEDDPKFSIPASFMMATITMTVYGGDIYRK----- 382
OY      239 QKRELELYKI-GITCY--LLGLIAMLVYLEPCELHELKK 275
Db      383 ---TLLGKIVGGICIAGVIALPIPIVNNSEFYKROK 420

RESULT 12
ID      C1KA_HUMAN          STANDARD;          PRT;          854 AA.
AC      Q14721;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DKH1).
GN      KCNB1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ikeda S.R., Soler F., Zuhlke R.D., Joho R.H., Lewis D.L.;
RL      Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC      ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC      CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC      MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC      WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC      GRADIENT.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC      CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC      EVERY THIRD POSITION.
CC      -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC      ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC      COMPARTMENTS.
CC      -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC      CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: L02840; AAA36156.1; -.
DR      MIM: 600397;
DR      INTERPRO: IPR000636; -.
DR      INTERPRO: IPR003091; -.
DR      Pfam: PF00520; Ion_trans. 1.
DR      PRINTS: PR00169; KCHANNEL.
KW      Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW      Glycoprotein; Multigene family; Phosphorylation.
FT      DOMAIN 1 182 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 183 204 SEGMENT S1 (POTENTIAL).
FT      DOMAIN 205 224 EXTRACELLULAR (POTENTIAL).

```


FT TRANSMEM 225 246 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 247 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 278 SEGMENT S3 (POTENTIAL).
 FT DOMAIN 279 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 312 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 327 348 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 349 388 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 389 410 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 411 854 CYTOPLASMIC (POTENTIAL).
 FT MOD.RES 440 440 PHOSPHORYLATION (HY CAPK)
 FT MOD.RES 440 440 (POTENTIAL).
 FT MOD.RES 492 492 PHOSPHORYLATION (HY CAPK)
 FT MOD.RES 492 492 (POTENTIAL).
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 854 AA: 95521 MW: 360DBE3E45731EDA CRC64;

Query Match 5.4%; Score 95; DB 1; Length 854;
 Best Local Similarity 21.7%; Pred. No. 6.3;
 Matches 61; Conservative 55; Mismatches 113; Indels 52; Gaps 14;

QY 13 LVERHSAMCFGLVGLVLYLVEGAVSSVELPYEDLLRDELRLKIKRRLLEEHCLE 72
 DB 174 LLEKPNSSVAAKILAIISIFIVLSTIALSLNTLP-----ELQSLD---EFGQSTDN 222
 QY 73 QOLEQFLGRVLEA-----SNYGVSVLSASGNMMMDFTSALFPASTVSTGYGHTVP 125
 DB 223 POLAH-----VEAVCIAMFTMETLRLPLSPK---KMKFKGPLMADLALIPYVYTF 274
 QY 126 LSDGKA---FCIIYVIGIPFTLLETAIVQRIIVHTRRPVLYFIHMGFSKOVAIV 182
 DB 275 LTSNNSVLOFQVNRVVOQ-FRIMRLRL-KLARHSTLOSLGFLRNSYML----- 327
 QY 183 HAVLGFVTVSCFFIIPAAVESVL-EDDNMFLE---SEYFCETSLSTIGLDVYPGEYGN 238
 DB 328 -GLIFLAMGIMFSSILVEFAEKDEDTFKSKIPASFWMTITMTVGYGDIYPRK---- 382
 QY 239 QKRELYKI--GITCY--LLGLIAMLYVETCELEHLEK 275
 DB 383 ---TLGKIVGGLCGIAGLVIALPLPIIVNNSFEYKEK 420

RESULT 13
 AG22_MOUSE STANDARD: PRT: 363 AA.
 ID AG22_MOUSE P35374;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE TYPE-2 ANGIOTENSIN II RECEPTOR (AT2).
 GN AGTR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-FETAL;
 RX MEDLINE-94092107; PubMed-8267573;
 RA Nakajima M., Mukoyama M., Pratt R.E., Horiiuchi M., Dzau V.J.;
 RT "Cloning of cDNA and analysis of the gene for mouse angiotensin II
 RT type 2 receptor.";
 RL Biochem. Biophys. Res. Commun. 197;393-399(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE-9412216; PubMed-8292631;
 RA Ichiki T., Herold C.L., Kamabayashi Y., Bardhen S., Inagami T.;
 RT "Cloning of the cDNA and the genomic DNA of the mouse angiotensin II
 RT type 2 receptor.";
 RL Biochim. Biophys. Acta 1189;247-250(1994).
 RN [3]
 RP SEQUENCE FROM N.A.

RX MEDLINE-96337434; PubMed-8726696;
 RA Nambias C., Cazaubon S.M., Sutren M., Masson M., Lazard D.,
 RA Villagros P., Elbaz N., Strosberg A.D.;
 RT "Molecular and functional characterization of angiotensin II AT2
 RT receptor in neuroblastoma NIE-115 cells.";
 RL Adv. Exp. Med. Biol. 396;167-173(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-LIVER;
 RX MEDLINE-95378283; PubMed-7650042;
 RA Horiiuchi M., Koike G., Yamada T., Mukoyama M., Nakajima M.,
 RA Dzau V.J.;
 RT "The growth-dependent expression of angiotensin II type 2 receptor is
 RT regulated by transcription factors interferon regulatory factor-1 and
 RT -2.";
 RL J. Biol. Chem. 270;20225-20230(1995).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MAY HAVE A ROLE IN CELL
 CC MORPHOGENESIS AND RELATED EVENTS IN GROWTH AND DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN FETUS, LOWER LEVELS IN ADULT
 CC BRAIN.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: S67465; AAB29336.1; -
 CC EMBL: U04828; AAC52128.1; -
 CC EMBL: U00766; AAC04933.1; -
 CC EMBL: L32840; AAB49539.1; ALT_INIT.
 CC EMBL: U11073; AAB48184.1; -
 CC PIR: JC2028; JC2028.
 CC HSSP: P34996; 1DD0.
 CC GCRDB: GCR_0890; -
 CC GCRDB: GCR_1007; -
 CC GCRDB: GCR_1010; -
 CC MGD: MGI:87966; AGTR2.
 CC INTERPRO: IPR000147; -
 CC INTERPRO: IPR000248; -
 CC INTERPRO: IPR000276; -
 CC PFM: PFM0001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PRINTS: PR00241; ANGIOTENSINR.
 CC PRINTS: PR00636; ANGIOTENSINR.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 CC PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; glycoprotein;
 CC Phosphorylation.
 CC
 CC FT DOMAIN 1 45
 CC FT TRANSMEM 46 71
 CC FT DOMAIN 72 80
 CC FT TRANSMEM 81 102
 CC FT DOMAIN 103 119
 CC FT TRANSMEM 120 140
 CC FT DOMAIN 141 160
 CC FT TRANSMEM 161 179
 CC FT DOMAIN 180 208
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 CC FT DOMAIN 314 363
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 CC FT CARBOHYD 13 13
 CC FT CARBOHYD 24 24
 CC FT CARBOHYD 29 29
 CC
 CC 1 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 2 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 3 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 4 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 5 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 6 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 7 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 5.4%; Score 94.5; DB 1; Length 363;
 Best Local Similarity 20.9%; Pred. No. 2.7;
 Matches 60; Conservative 40; Mismatches 80; Indels 107; Gaps 16;

CC 17 HRSAMCEGFL--VLGYLLYL-VFGAVF--SSVELPYEDJLNOELRLKRLRELEH-- 67
 DB 106 YRDWLEFGPYMKCVGSEFLNMFASIFITCKMSVD-RYSVITPILSQNRNPMQASVYV 164
 QY 68 -----ECLEEQLEQFLGVLEASNY-----GVSYLSNAGSNMN 101
 DB 165 PLVWCMACLS--SLPTFFFDVRIEFLGVNACIMAPPEKRYQMSAGIALMKNIILG--- 219
 QY 102 WDFTSALFFAST-----VLSTGCGHVPISDS---GFAFCIYSVIGIPE-TLLE 148
 DB 220 --FIPLIFATATCFPIGRKLKLTNSYGNRRITRDVYKMAAVLAFITICWLPFHVLT 277
 QY 149 LTAIVORITVHTVRPVLVYEHIRWGSKQVAVI---HAVLIGFVYSCFFPIPAV 203
 DB 278 LDALTWMMGIIN-----SCEVIAVIDLALPFAJILIGF-TNCG----- 312
 QY 204 SYLEDMMNLESEFFCFISLTIGLDYVGEQYNQFRELKIGIT 250
 DB 313 -----VNPFYXCFV-----GNRFQOKLRSEVFRVPI 338

RESULT 15
 ID C104_HUMAN STANDARD; PRT; 695 AA.
 AC P56696; O96025;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KOT-LIKE 4.
 GN KCNQ4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RX MEDLINE=99148276; PubMed=10025409;
 RA Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
 RA El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;
 RT "KCNQ4, a novel potassium channel expressed in sensory outer hair
 RT cells, is mutated in dominant deafness.";
 RL Cell 96:437-446(1999).
 RN [2]
 RX VARIANTS DENA2 SER-276; CYS-285 AND SER-321.
 RX MEDLINE=99299248; PubMed=10369879;
 RA Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schatteman I.,
 RA Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Deciau F.,
 RA Maertens H., Kastyur K., Bhasin S., McGulirt W.T., Smith R.J.H.,
 RA Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
 RA Van Camp G.;
 RT "Mutations in the KCNQ4 gene are responsible for autosomal dominant
 RT deafness in four DENA2 families.";
 RL Hum. Mol. Genet. 8:1321-1328(1999).
 CC -1- FUNCTION: MAY BE RESPONSIBLE FOR POTASSIUM IONS AFTER STIMULATION
 CC OF THE HAIR CELL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
 CC SENSORY HAIR CELLS OF THE COCHLEA.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF AUTOSOMAL DOMINANT
 CC NONSYNDROMIC SENSORINEURAL DEAFNESS TYPE 2 (DENA2).
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. KOT SUBFAMILY.
 CC -----
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CC -----
 DR EMBL; AF105202; AAD14680.1; -;
 DR EMBL; AF105216; AAD14681.1; -;
 DR EMBL; AF105203; AAD14681.1; JOINED.
 DR EMBL; AF105204; AAD14681.1; JOINED.
 DR EMBL; AF105205; AAD14681.1; JOINED.
 DR EMBL; AF105206; AAD14681.1; JOINED.
 DR EMBL; AF105207; AAD14681.1; JOINED.
 DR EMBL; AF105208; AAD14681.1; JOINED.
 DR EMBL; AF105209; AAD14681.1; JOINED.
 DR EMBL; AF105210; AAD14681.1; JOINED.
 DR EMBL; AF105211; AAD14681.1; JOINED.
 DR EMBL; AF105212; AAD14681.1; JOINED.
 DR EMBL; AF105213; AAD14681.1; JOINED.
 DR EMBL; AF105214; AAD14681.1; JOINED.
 DR EMBL; AF105215; AAD14681.1; JOINED.
 DR MIM; 603537; -;
 DR MIM; 600101; -;
 DR INTERPRO; IPR000636; -;
 DR INTERPRO; IPR003091; -;
 DR PFAM; PF00520; Ion.trans. 1.
 DR PRINTS; PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Multigene family; Disease mutation; Deafness.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 98 118 POTENTIAL.
 FT TRANSMEM 132 152 POTENTIAL.
 FT TRANSMEM 173 193 POTENTIAL.
 FT TRANSMEM 238 258 POTENTIAL.
 FT TRANSMEM 298 318 POTENTIAL.
 FT VARIANT 276 276 W -> S (IN DENA2).
 FT VARIANT 285 285 G -> C (IN DENA2). LOSS OF POTASSIUM
 FT SELECTIVITY OF THE PORE).
 FT VARIANT 285 285 /FTID=VAR.008727.
 FT VARIANT 285 285 G -> S (IN DENA2).
 FT VARIANT 321 321 /FTID=VAR.001547.
 FT VARIANT 321 321 G -> S (IN DENA2).
 FT VARIANT 321 321 /FTID=VAR.008728.
 SQ SEQUENCE 695 AA; 77091 MW; A58737BD845E1A3A CRC64;

Query Match 5.4%; Score 94; DB 1; Length 695;
 Best Local Similarity 21.7%; Pred. No. 6;
 Matches 70; Conservative 46; Mismatches 108; Indels 98; Gaps 17;

CC 6 AGSC-----VLRVHRSAMCEGFLVGLLYLVFGAVFSSVELP 47
 DB 65 SGSACGGRSSAAHRRYRLQWVYVLEPRR-GWAFYHV--FIPLVFSLVSLVSTI 121
 QY 48 YEDLLRELRLKRLFLDEHCEQLEQFLGVLEASNYGVSLSNAS-----GNNWMD 103
 DB 122 OE--HOEL-----ANECL--LLEFVMIVVGELEIVRWASGCCCRRYRQGR 166
 QY 104 FTSALFFASTVLTSTGTHVPLSDGKAFCIITSVIGIPIPTL-----LFLFAVQ 154
 DB 167 FRFA-----RKPCVIDEIFYFVASVAVIAGTGNIFATSAKR 204
 QY 155 RI-----TVHVTRR-----PVLXPHIRWGSKQVAVIAVALLGF-VTVSCFF 198
 DB 205 SMRLQLILRWMDRMRRCGTWKLGSVYAH-----SKELT--AWYIGFLVLFASFV 256
 QY 199 PAATFVLEDMMNLESEFFCFISLTIGLDYVGEQYNQFRELK-IGITCYLL-IG 256
 DB 257 YLAEKDANSDFSSYADSLMWGTITLTTIGYGDKTPHWLGVLAAGFALGISFPALPAG 316
 QY 257 LIAMLVLEFCEELHELEKFRK 278

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Db 317 ILGSGFALKV-OEQHROKHPEK 337

Search completed: February 14, 2001, 03:43:05
Job time: 28254 sec
